STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/516,361A_

Source: _PCT/0_

Date Processed by STIC: _1/13/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/516, 36/A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
Wrapped Aminos was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length The rules require that a line **not exceed 72** characters in length. This includes white spaces.

3 ____ Misaligned Amino The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
Numbering use **space characters**, instead.

4 ✓ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
"bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences Sequence(s) ____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
(NEW RULES) <210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or **Xaa** represents.

10 ____ Invalid <213> Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
Response scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
"bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa "n" can **only** represent a single <u>nucleotide;</u> "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 01/13/2006
PATENT APPLICATION: US/10/516,361A   TIME: 10:50:50

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\01132006\J516361A.raw

see item 4 on Error Summary Sheet

```
  2 <110> APPLICANT: Islam Amirul
  3         Hazra Papia
  5 <120> TITLE OF INVENTION: An improved method of detection of target nucleic acid
sequence by
  6         nucleic acid amplification
  8 <130> FILE REFERENCE: 3875.033
 10 <140> CURRENT APPLICATION NUMBER: US 10/516,361A
C-->11 <141> CURRENT FILING DATE: 2004-11-30
 13 <150> PRIOR APPLICATION NUMBER: PCT/IN 03/00204
W-->14 <151> PRIOR FILING DATE: (2003.05.30) 2003-05-30
 16 <150> PRIOR APPLICATION NUMBER: 487/MUM/2002 (IN)
W-->17 <151> PRIOR FILING DATE: (2002.05.31) 2002-05-31
 19 <160> NUMBER OF SEQ ID NOS: 31
```

use this format for dates

ERRORED SEQUENCES

invalid response (see item 10 on Error Summary Sheet)

Does Not Comply
Corrected Diskette Needed

```
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 20
 23 <212> TYPE: DNA
E-->24 <213> ORGANISM: Artificial / Unknown Sequence
 26 <220> FEATURE:
 27 <221> NAME/KEY: primer_bind
 28 <222> LOCATION:
 29 <223> OTHER INFORMATION: Forward PCR primer for amplification of a target
 30         sequence chosen arbitrarily and made from sequence
 31         IDs 3 &4.
 33 <400> SEQUENCE: 1
 34 acttaagtta   gagcgtttgc           20
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 20
 39 <212> TYPE: DNA
E-->40 <213> ORGANISM: Artificial / Unknown Sequence
 42 <220> FEATURE:
 43 <221> NAME/KEY: primer_bind
 44 <222> LOCATION:
 45 <223> OTHER INFORMATION: Reverse PCR primer for amplification of a target
 46         sequence chosen arbitrarily and made from sequence
 47         IDs 3 &4.
 49 <400> SEQUENCE: 2
 50 tggtagtatg   tgatttagtc           20
 53 <210> SEQ ID NO: 3
 54 <211> LENGTH: 40
 55 <212> TYPE: DNA
```

same error

RAW SEQUENCE LISTING   DATE: 01/13/2006
PATENT APPLICATION: US/10/516,361A   TIME: 10:50:50

Input Set : A:\pto.da.txt
Output Set: N:\CRF4\01132006\J516361A.raw

```
E--> 56 <213> ORGANISM: Artificial / Unknown Sequence
     58 <220> FEATURE:
     59 <221> NAME/KEY: misc_difference
     60 <222> LOCATION:                              Bases
     61 <223> OTHER INFORMATION: Arbitrarily chosen sequence. Base 27 to 40 are
     62       complementary to basis 31 to 44 of sequence ID 4.
     63       DNA polymerase extention of annealed Sequence IDs 3        extension
     64       & 4 results in the target sequence
     66 <400> SEQUENCE: 3
     67 tacacttaag  ttagagcgtt  tgcgcccact  acgacggttg        40
     71 <210> SEQ ID NO: 4
     72 <211> LENGTH: 44
     73 <212> TYPE: DNA
E--> 74 <213> ORGANISM: Artificial / Unknown Sequence
     76 <220> FEATURE:
     77 <221> NAME/KEY: misc_difference
     78 <222> LOCATION:                              Bases
     79 <223> OTHER INFORMATION: Arbitrarily chosen sequence. Base 27 to 40 are
     80       complementary to basis 31 to 44 of sequence ID 4.
     81       DNA polymerase extention of annealed Sequence IDs 3
     82       & 4 results in the target sequence
     84 <400> SEQUENCE: 4
E--> 85 gttttttgtgg  tagtatgtga  tttagtcatt  caaccgtcgt  agtg     44 (see item 1 on
     86    44                                                          Error Summa
                                                                       Sheet)
     89 <210> SEQ ID NO: 5
     90 <211> LENGTH: 20
     91 <212> TYPE: DNA
E--> 92 <213> ORGANISM: Artificial / Unknown Sequence
     94 <220> FEATURE:
     95 <221> NAME/KEY: primer_bind
     96 <222> LOCATION:
     97 <223> OTHER INFORMATION: Forward PCR primer for amplification of a target
     98       sequence chosen arbitrarily and made from sequence
     99       IDs 3 &4. Base t at base position 18 from 5' end is having
    100        fluorophore FAM
    102 <400> SEQUENCE: 5
    103 acttaagtta  gagcgtttgc        20
```

see pp 3-5 for more error

Input Set : **A:\pto.da.txt**
Output Set: **N:\CRF4\01132006\J516361A.raw**

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:17 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:24 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial"
and "Unknown" for SEQ ID#:1
L:40 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial"
and "Unknown" for SEQ ID#:2
L:56 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial"
and "Unknown" for SEQ ID#:3
L:74 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial"
and "Unknown" for SEQ ID#:4
L:85 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:44 SEQ:4
L:92 M:251 E: Invalid Description for Numeric Identifier, <213> ORGANISM has both "Artificial"
and "Unknown" for SEQ ID#:5
L:112 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:125 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:141 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:155 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:169 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:183 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:197 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:211 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:225 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:239 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:253 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:267 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:281 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:295 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:309 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:325 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:341 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:356 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:371 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:386 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:401 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:416 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:431 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:446 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
L:461 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30
L:475 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
L:483 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:485 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:485 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:14
L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:486 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5